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	*	20	*	40	*	60
0826 :	--	MRVFAISINQKVCDDIFGLVFRDITTLNSINATHHQAQIFDAISKTFEGGL :				52
lex2b :	--	----- MFTPTFLNLEASIDRKAYMOQFELFSNN- -----				32
llob1 :	MNQSI	NQSI	NQSI	NQSI	NQSVIVLVAERHSHOFAFOHP :	69
lgtB :	--	----- MONHVLSLASRGR--RAHQ-ADTGR-				25

	*	80	*	100	*	120	*	1
0826	:	HPVYKXHLHPYFTTQNIK	MGCTTN	LISEVSKFYATK	YHAKFMS	LTGELG	GYASHY	SLWEKCIETNEA-
lex2b	:	-LIQETIHFDATYKSNPNHP	LEORYN	---ENKRLN	KAGYD	---LTLG	QGLGYASHY	SMWEKCVLEIYLP-
lob1	:	DIVINYQFTGWNGLQPNHPL	LEAKIN	---KQKQNR	QKRGNE	---ITL	GQGLGYASHY	LLWEKCVQIQOP-
lgtb	:	-GTPQEDDALM	---PSEPLEQ	ANVA	---ELVPGIS	AHP	YLSGVEKACFM	SHAVLWIKQALDEGLPY

	40	*	160	*	180	*	200	
0826 :	ICIGEDDITL---	KEDHKEGDDTLEKHQI	ELGYIRLMLLLDASV	KSEPLSHKNHEIQER	SGITKANS	:	185	
lex2b :	IIVLEDDAKF---	GNPFEVDEFLNDKN	TFEEFKLLP	PRNNRR	ELSTGCHLSVYFSK	:	152	
lob1 :	IIVLEDDAIL---	QNPFLAYQCFCAEN	QDFEFLHSHVSSKPT	---	IITHLPLSTKKEHYF	:	192	
19tb :	IIVLEDDVLEGEER	FLNEDAWQERFDP	DTAFIVRLNEMFHL	LSPS---	GVADYCGRAPPLLES	:	148	

	*	220	*	240	*	260	*				
0826 :	EGVGHQGV	LIIPKIANVFLK	---	CSFKWV	PVDITM	---	DATFIHGVKNVLOP	EVMAH	U	: 239	
lex2b :	GFACATGV	LTPOARKELT	---	OSKEMV	PLVDITM	---	DREFFENV	PPVAIVP	DLCTER	DG : 207	
lob1 :	GYSN	HTGV	LTPOAAOKFLD	---	SSQEW	YNVDIFM	---	DREYENHVAIK	GVNP	PCVKRP	DF : 247
19tB :	EHWC	TAGV	LSKMWTFEL	DRFAAL	PPEGLHP	VDLMMFS	DDFFDREG	MBVCLNP	PALCAOCEI	HYAKPHDQ	: 217

		280	*	300	*	320	*	
0826	:	--EQISTIAK	----	EPY	----	SPKALWRELFHK	----	YIKWGHV
lex2b	:	--EIESIIVEQ	----	KQR	----	SLKIVIRELENL	----	YTNKRLNLFH
lob1	:	--SKQSITMN	----	KNR	----	TEWKLREYFAL	----	LEFIRELVWTCYC
19tB	:	NSAIGSLIEHDLRLNR	----	QORDSPANTEKHLRRLAL	----	KTSREREXRPRRQ	----	LEFIRELVWTCYC

Fig. 1

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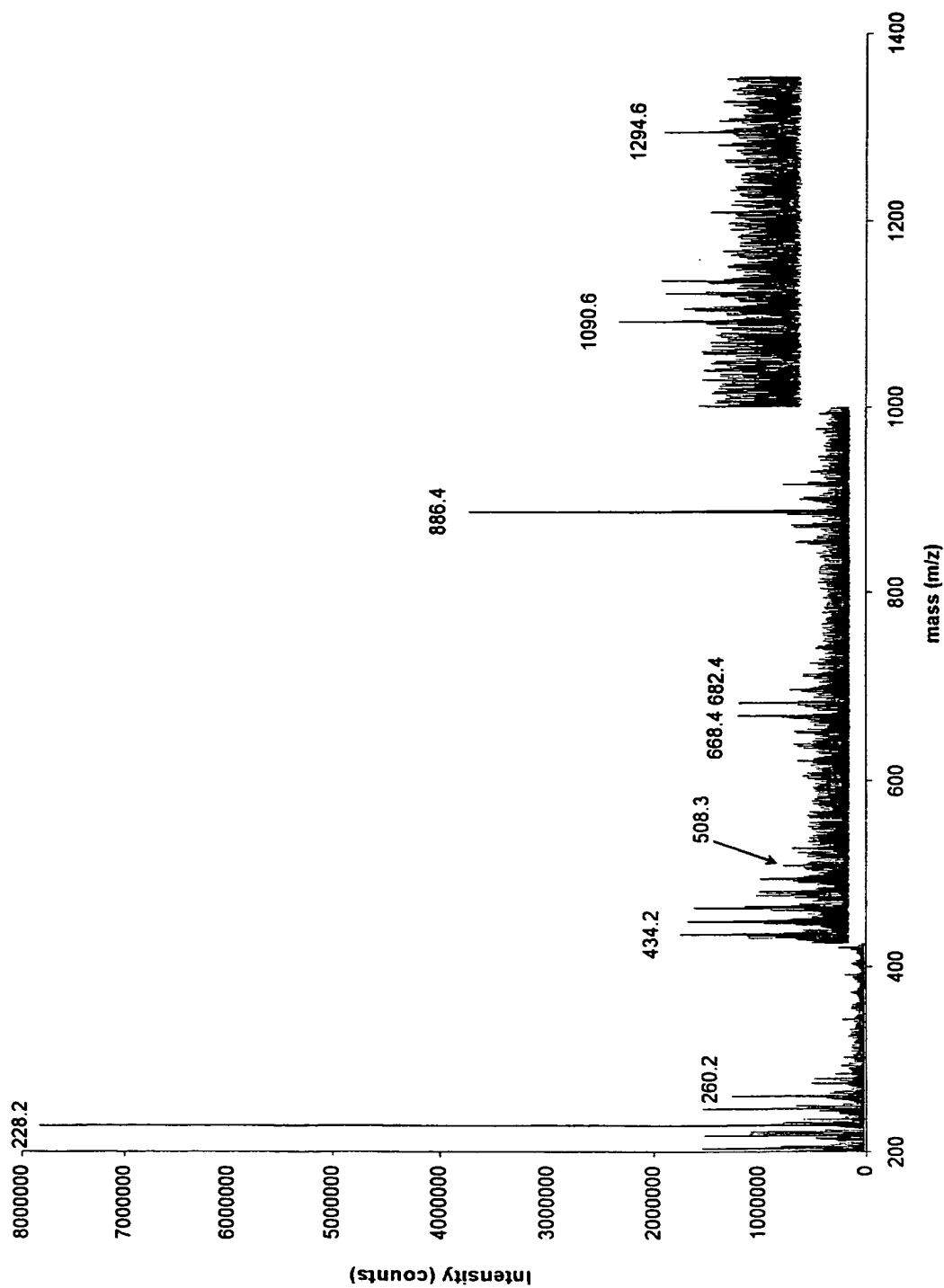
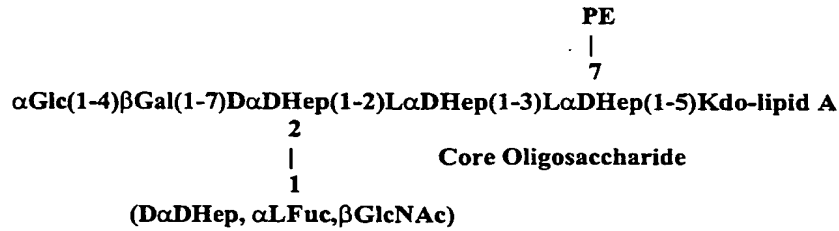


Fig. 2

Fig. 3

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H. pylori HP0159 mutant lipopolysaccharides of strains 26695 and SS1 .



H. pylori HP0479 mutant lipopolysaccharides of strains 26695 and SS1.

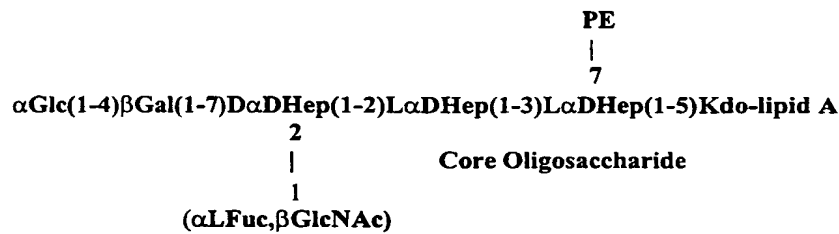


Fig. 3 (Cont.)

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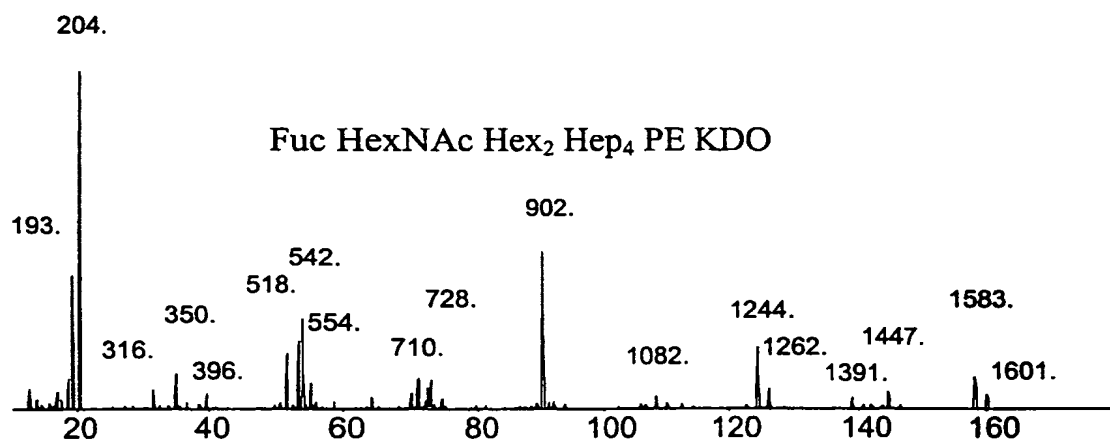


Fig. 4

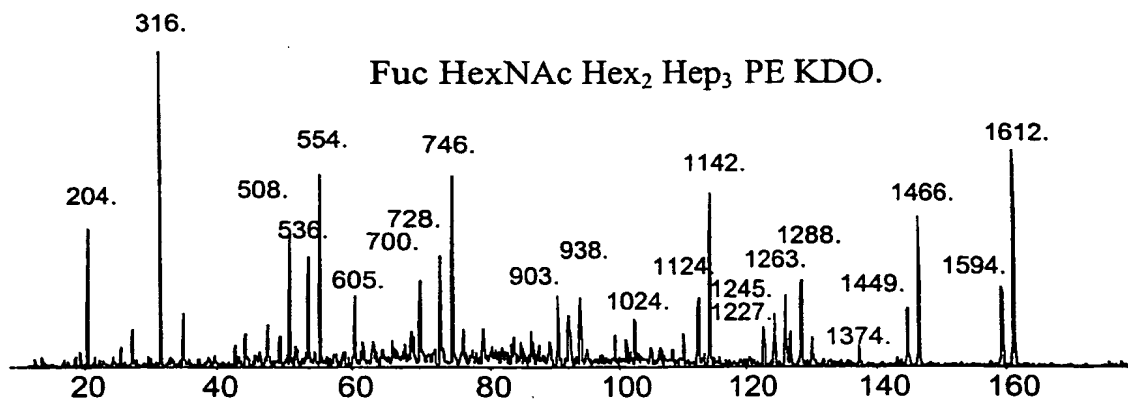


Fig. 5